

(11)

Untitled

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ttcataacaa aggactatcc tccttgcata aaatttctaa gacgaaaaat ccct atg 177
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aat cta gtt gat gaa ctt ctt ctc atc ttg gtt aaa gac agt att ttc 273
Asn Leu Val Asp Glu Leu Leu Leu Ile Leu Val Lys Asp Ser Ile Phe
20 25 30
act caa gta ata aaa ggc gag gga aag aca gaa tta aaa gac ata ctt 321
Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu
35 40 45
aca gac aac act ggt aag ttt aaa gaa ctt ata gaa agt gca ggt aaa 369
Thr Asp Asn Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys
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Asp Ile Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly
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Leu Ile Glu Gly Asn Gly Lys Thr Glu Ala Lys Glu Val Arg Thr Asn
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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 4

<211> LENGTH: 849

<212> TYPE: PRT

<213> ORGANISM: Ehrlichia risticii

<400> SEQUENCE: 4

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Glu	Leu	Phe	Thr	Asp	Ala	Thr	Lys	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu
Thr	Asn	Asp	Thr	Ala	Lys	Glu	Ile	Leu	Thr	Asp	Gln	Thr	Ala	Lys	Glu
Val	Leu	Lys	Asp	Gly	Thr	Ala	Lys	Asp	Ile	Leu	Lys	Asp	Thr	Asn	Ala
Arg	Ala	Leu	Leu	Lys	Asp	Ser	Thr	Ala	Lys	Glu	Val	Leu	Lys	Cys	Asp
Lys	Phe	Lys	Glu	Ala	Ile	Thr	Gly	Ala	Gly	Lys	Asp	Glu	Leu	Lys	Tyr
Ile	Leu	Thr	Asn	Ser	Glu	Phe	Lys	Ser	Leu	Phe	His	Ser	Lys	Asp	Ser
Ala	Glu	Ala	Val	Lys	Ala	Ile	Phe	Thr	His	Asn	Lys	Phe	Lys	Glu	Leu
Leu	Glu	His	Ala	Arg	Thr	Thr	Gln	Thr	Ile	Arg	Arg	Arg	Phe	Ala	Asn
Ala	Leu	Asp	Gln	Leu	Lys	Ala	Leu	Ile	Thr	Cys	Gly	Ser	Gly	Asp	His
Ala	Thr	Lys	Leu	Gln	Ala	Phe	Gly	Ser	Ala	Leu	Cys	Thr	Lys	Lys	Lys
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Ala

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 5

<211> LENGTH: 1937

<212> TYPE: DNA

<213> ORGANISM: Ehrlichia risticii

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (175)..(1791)

<400> SEQUENCE: 5

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tttataacaa	aggactaccc	tcctacata	aaatttctaa	gacgaaaaat	ccct atg	177
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					1	
tca aat gaa aca ctt ctg agc gta ctt tct gat gaa acg cac ttt gct						225
Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala						
	5		10		15	
aat cta gtt gat gaa ctt ctt ctc agc ttg gtt aaa gac agt att ttc						273
Asn Leu Val Asp Glu Leu Leu Leu Ser Leu Val Lys Asp Ser Ile Phe						
	20		25		30	
act caa gta ata aaa ggc gag gga aag aca gaa tta aaa gac att ctt						321
Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu						
	35		40		45	
aca gat agc act ggc aag ttt aaa gag ctg ata gga agt agc ggt aag						369
Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly Lys						
	50		55		60	
gat ata cta aaa agc ata cac aca gat ggc tca ggc aac ttt aaa ggc						417
Asp Ile Leu Lys Ser Ile His Thr Asp Gly Ser Gly Asn Phe Lys Gly						
	70		75		80	
ctt ata caa agc aca ggt aag gca gaa gta aaa gag gta ctc act aat						465

Untitled																
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Glu	Lys	Phe	Lys	Glu	Leu	Phe	Gly	Ser	Glu	Gly	Lys	Asp	Ile	Leu	Lys	
		100					105					110				
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Glu	Ile	Leu	Thr	Asp	Asn	Thr	Gly	Asn	Phe	Lys	Gly	Leu	Ile	Glu	Gly	
	115					120					125					
aaa	ggt	aag	gat	gaa	gca	aag	gga	gta	ctt	act	gac	gag	aaa	ttt	aaa	609
Lys	Gly	Lys	Asp	Glu	Ala	Lys	Gly	Val	Leu	Thr	Asp	Glu	Lys	Phe	Lys	
130				135						140					145	
ggc	ttg	ttt	gat	gac	aaa	aca	ata	gct	ggc	tat	gta	aaa	gaa	ata	ctc	657
Gly	Leu	Phe	Asp	Asp	Lys	Thr	Ile	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu	
			150					155						160		
acc	agc	gag	agt	tta	aaa	aac	tgt	ttg	aaa	ggt	gca	ggt	aag	act	aaa	705
Thr	Ser	Glu	Ser	Leu	Lys	Asn	Cys	Leu	Lys	Gly	Ala	Gly	Lys	Thr	Lys	
			165				170						175			
gta	aaa	gaa	ctc	ctc	att	gat	gag	aag	ttt	caa	aaa	tta	ttt	gag	gat	753
Val	Lys	Glu	Leu	Leu	Ile	Asp	Glu	Lys	Phe	Gln	Lys	Leu	Phe	Glu	Asp	
		180					185					190				
gac	acg	aaa	gcc	agt	cat	gta	aaa	gaa	ata	ctt	aca	gac	agt	aac	gct	801
Asp	Thr	Lys	Ala	Ser	His	Val	Lys	Glu	Ile	Leu	Thr	Asp	Ser	Asn	Ala	
	195				200					205						
aag	gaa	ata	ctc	aca	aat	gaa	gta	gca	aaa	gag	gta	cta	aaa	tcc	gat	849
Lys	Glu	Ile	Leu	Thr	Asn	Glu	Val	Ala	Lys	Glu	Val	Leu	Lys	Ser	Asp	
210				215						220					225	
aaa	ttt	aaa	gat	gca	ata	act	ggt	gct	ggt	aag	gac	gca	cta	aaa	gag	897
Lys	Phe	Lys	Asp	Ala	Ile	Thr	Gly	Ala	Gly	Lys	Asp	Ala	Leu	Lys	Glu	
			230					235					240			
ata	ctt	act	tgc	gat	aaa	ttt	aaa	gat	gca	gta	aca	ggt	aat	ggt	aag	945
Ile	Leu	Thr	Cys	Asp	Lys	Phe	Lys	Asp	Ala	Val	Thr	Gly	Asn	Gly	Lys	
			245					250					255			
gac	gca	cta	aaa	gaa	ata	ctt	act	tgc	gat	aaa	ttt	aaa	gat	gca	gta	993
Asp	Ala	Leu	Lys	Glu	Ile	Leu	Thr	Cys	Asp	Lys	Phe	Lys	Asp	Ala	Val	
	260						265					270				
aca	ggc	aat	ggt	aaa	gac	aag	cta	aaa	gag	att	ctt	act	cac	gag	aag	1041
Thr	Gly	Asn	Gly	Lys	Asp	Lys	Leu	Lys	Glu	Ile	Leu	Thr	His	Glu	Lys	
	275					280					285					
ttt	aaa	gca	ctc	ata	gag	agt	gaa	ggc	aaa	gac	ata	ctg	aaa	gaa	att	1089
Phe	Lys	Ala	Leu	Ile	Glu	Ser	Glu	Gly	Lys	Asp	Ile	Leu	Lys	Glu	Ile	
290				295						300					305	
ctt	aca	gat	agt	acc	ggt	aaa	ttt	aaa	gag	cta	ata	gaa	agc	act	ggt	1137
Leu	Thr	Asp	Ser	Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Glu	Ser	Thr	Gly	
			310						315					320		
aaa	gac	aag	cta	aaa	gag	att	ttc	aca	gat	aac	acc	ggt	aac	ttt	aaa	1185
Lys	Asp	Lys	Leu	Lys	Glu	Ile	Phe	Thr	Asp	Asn	Thr	Gly	Asn	Phe	Lys	
			325					330					335			
ggg	ctt	gta	gaa	ggc	gcc	ggt	aag	gat	gaa	gca	aaa	gca	gta	ctt	act	1233
Gly	Leu	Val	Glu	Gly	Ala	Gly	Lys	Asp	Glu	Ala	Lys	Ala	Val	Leu	Thr	
	340					345						350				
cac	gag	aaa	ttt	aaa	gac	ttg	ttt	aat	gac	aaa	aca	aca	gct	ggc	tac	1281
His	Glu	Lys	Phe	Lys	Asp	Leu	Phe	Asn	Asp	Lys	Thr	Ala	Gly	Tyr		
	355					360					365					
gtg	aaa	gaa	ata	ctc	acc	agt	gat	aag	ttt	aaa	aaa	tta	ttt	gag	gac	1329
Val	Lys	Glu	Ile	Leu	Thr	Ser	Asp	Lys	Phe	Lys	Lys	Leu	Phe	Glu	Asp	
370				375						380					385	
aat	acc	aaa	gct	ggc	tac	gtg	aaa	gaa	ata	ctc	acg	aac	gat	aca	gct	1377

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Asn	Thr	Lys	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu	Thr	Asn	Asp	Thr	Ala	
				390					395					400		
aag	gaa	ata	ctc	aca	aat	caa	aca	gct	aaa	gaa	gtc	cta	aaa	gac	agc	1425
Lys	Glu	Ile	Leu	Thr	Asn	Gln	Thr	Ala	Lys	Glu	Val	Leu	Lys	Asp	Ser	
			405					410					415			
aca	gcc	aaa	gaa	ata	cta	aaa	tgc	gat	aaa	ttt	aag	gac	gca	ata	aca	1473
Thr	Ala	Lys	Glu	Ile	Leu	Lys	Cys	Asp	Lys	Phe	Lys	Asp	Ala	Ile	Thr	
		420					425					430				
ggc	gct	ggg	aaa	gat	gag	cta	aaa	tac	ata	ctc	act	aat	aac	gag	ttt	1521
Gly	Ala	Gly	Lys	Asp	Glu	Leu	Lys	Tyr	Ile	Leu	Thr	Asn	Asn	Glu	Phe	
	435					440				445						
aaa	agc	tta	ttt	gat	agc	aaa	gat	agc	gct	gaa	gct	gtt	aaa	gca	ata	1569
Lys	Ser	Leu	Phe	Asp	Ser	Lys	Asp	Ser	Ala	Glu	Ala	Val	Lys	Ala	Ile	
450				455					460					465		
ttt	acc	cac	aat	aag	ttt	aaa	gaa	cta	ctt	aaa	acg	tgc	aag	gac	aac	1617
Phe	Thr	His	Asn	Lys	Phe	Lys	Glu	Leu	Leu	Lys	Thr	Cys	Lys	Asp	Asn	
			470					475					480			
cca	aaa	aat	acg	gcg	gcg	ctt	gca	gct	gct	tta	gat	gaa	cta	aaa	gat	1665
Pro	Lys	Asn	Thr	Ala	Ala	Leu	Ala	Ala	Ala	Leu	Asp	Glu	Leu	Lys	Asp	
			485					490					495			
cta	att	acg	tgt	gac	cg	aat	aat	cat	gca	aca	aaa	cta	caa	gcc	ttt	1713
Leu	Ile	Thr	Cys	Asp	Arg	Asn	Asn	His	Ala	Thr	Lys	Leu	Gln	Ala	Phe	
		500					505					510				
gga	agt	gca	cta	tgc	acc	aga	aaa	aaa	gag	tcg	tgc	gat	aat	ttt	agc	1761
Gly	Ser	Ala	Leu	Cys	Thr	Arg	Lys	Lys	Glu	Ser	Cys	Asp	Asn	Phe	Ser	
	515					520				525						
cct	gca	agc	tgc	agt	agt	aca	gca	gct	aca	taattacgta	gcgctaggtg					1811
Pro	Ala	Ser	Cys	Ser	Ser	Thr	Ala	Ala	Thr							
530					535											
ggggtaaatt	acccccac	ct	acgtaga	atc	acacgggg	gaa	ctttctctct	attactgagg								1871
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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 6

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Ehrlichia risticii

<400> SEQUENCE: 6

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		20						25				30				
Phe	Thr	Gln	Val	Ile	Lys	Gly	Glu	Gly	Lys	Thr	Glu	Leu	Lys	Asp	Ile	
		35				40					45					
Leu	Thr	Asp	Ser	Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Gly	Ser	Ser	Gly	
	50				55				60							
Lys	Asp	Ile	Leu	Lys	Ser	Ile	His	Thr	Asp	Gly	Ser	Gly	Asn	Phe	Lys	
65				70					75				80			
Gly	Leu	Ile	Gln	Ser	Thr	Gly	Lys	Ala	Glu	Val	Lys	Glu	Val	Leu	Thr	
		85						90					95			
Asn	Glu	Lys	Phe	Lys	Glu	Leu	Phe	Gly	Ser	Glu	Gly	Lys	Asp	Ile	Leu	
		100					105					110				
Lys	Glu	Ile	Leu	Thr	Asp	Asn	Thr	Gly	Asn	Phe	Lys	Gly	Leu	Ile	Glu	
	115						120					125				
Gly	Lys	Gly	Lys	Asp	Glu	Ala	Lys	Gly	Val	Leu	Thr	Asp	Glu	Lys	Phe	
	130					135				140						
Lys	Gly	Leu	Phe	Asp	Asp	Lys	Thr	Ile	Ala	Gly	Tyr	Val	Lys	Glu	Ile	

Untitled

145	Leu	Thr	Ser	Glu	Ser	150	Leu	Lys	Asn	Cys	155	Leu	Lys	Gly	Ala	Gly	160	Lys	Thr
	Lys	Val	Lys	Glu	165	Leu	Leu	Ile	Asp	Glu	170	Lys	Phe	Gln	Lys	Leu	175	Phe	Glu
	Asp	Asp	Thr	180	Ala	Ser	His	Val	185	Lys	Glu	Ile	Leu	Thr	190	Asp	Ser	Asn	
	Ala	Lys	Glu	Ile	Leu	Thr	Asn	Glu	200	Val	Ala	Lys	Glu	Val	Leu	Lys	Ser		
	Asp	Lys	Phe	Lys	Asp	Ala	Ile	Thr	215	Gly	Ala	Gly	Lys	Asp	Ala	Leu	Lys		
225	Glu	Ile	Leu	Thr	Cys	230	Asp	Lys	Phe	Lys	Asp	Ala	Val	Thr	Gly	Asn	Gly		
	Lys	Asp	Ala	Leu	Lys	Glu	Ile	Leu	Thr	Cys	250	Asp	Lys	Phe	Lys	Asp	Ala		
	Val	Thr	Gly	Asn	Gly	Lys	Asp	Lys	Leu	Lys	Glu	Ile	Leu	Thr	His	Glu			
	Lys	Phe	Lys	Ala	Leu	Ile	Glu	Ser	Glu	Gly	Lys	Asp	Ile	Leu	Lys	Glu			
	Ile	Leu	Thr	Asp	Ser	Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Glu	Ser	Thr			
305	Gly	Lys	Asp	Lys	Leu	Lys	Glu	Ile	Phe	Thr	Asp	Asn	Thr	Gly	Asn	Phe			
	Lys	Gly	Leu	Val	Glu	Gly	Ala	Gly	Lys	Asp	Glu	Ala	Lys	Ala	Val	Leu			
	Thr	His	Glu	Lys	Phe	Lys	Asp	Leu	Phe	Asn	Asp	Lys	Thr	Thr	Ala	Gly			
	Tyr	Val	Lys	Glu	Ile	Leu	Thr	Ser	Asp	Lys	Phe	Lys	Lys	Leu	Phe	Glu			
	Asp	Asn	Thr	Lys	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu	Thr	Asn	Asp	Thr			
385	Ala	Lys	Glu	Ile	Leu	Thr	Asn	Gln	Thr	Ala	Lys	Glu	Val	Leu	Lys	Asp			
	Ser	Thr	Ala	Lys	Glu	Ile	Leu	Lys	Cys	Asp	Lys	Phe	Lys	Asp	Ala	Ile			
	Thr	Gly	Ala	Gly	Lys	Asp	Glu	Leu	Lys	Tyr	Ile	Leu	Thr	Asn	Asn	Glu			
	Phe	Lys	Ser	Leu	Phe	Asp	Ser	Lys	Asp	Ser	Ala	Glu	Ala	Val	Lys	Ala			
	Ile	Phe	Thr	His	Asn	Lys	Phe	Lys	Glu	Leu	Leu	Lys	Thr	Cys	Lys	Asp			
465	Asn	Pro	Lys	Asn	Thr	Ala	Ala	Leu	Ala	Ala	Leu	Asp	Glu	Leu	Gln	Ala			
	Asp	Leu	Ile	Thr	Cys	Asp	Arg	Asn	Asn	His	Ala	Thr	Lys	Leu	Gln	Ala			
	Phe	Gly	Ser	Ala	Leu	Cys	Thr	Arg	Lys	Lys	Glu	Ser	Cys	Asp	Asn	Phe			
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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 7

<211> LENGTH: 1791

<212> TYPE: DNA

<213> ORGANISM: Ehrlichia risticii

<220> FEATURE:

<221> NAME/KEY: CDS

Untitled

<222> LOCATION: (175)..(1677)

<400> SEQUENCE: 7

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ttcataacaa	aggactatcc	tccttgcata	aaattttctaa	gacgaaaaat	cctt atg		177
					Met		
					1		
tca aat gaa aca ctt ctg agc gta ctt tct gat gaa acg cac ttt gct							225
Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala							
	5		10		15		
aat cta gtt gat gaa ctt ctt ctc agc ttg gtt aaa gac agt att ttc							273
Asn Leu Val Asp Glu Leu Leu Leu Ser Leu Val Lys Asp Ser Ile Phe							
	20		25		30		
act caa gta ata aaa ggc gag gga aag aca gaa tta aaa gac att ctt							321
Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu							
	35		40		45		
aca gat agc act ggc aag ttt aaa gag ctg ata gga agt agc ggt aag							369
Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly Lys							
	50		55		60		65
gat ata cta aaa agc ata ctc aca gat ggc tca ggc aac ttt aaa ggc							417
Asp Ile Leu Lys Ser Ile Leu Thr Asp Gly Ser Gly Asn Phe Lys Gly							
	70		75		80		
ctt ata caa agc aca ggt aag gca gaa gta aaa gag gta ctc act aat							465
Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr Asn							
	85		90		95		
gaa aaa ttc aaa gag ctt ttt gga agc gat ggt aag gat ata tta aaa							513
Glu Lys Phe Lys Glu Leu Phe Gly Ser Asp Gly Lys Asp Ile Leu Lys							
	100		105		110		
gac ata ctc aca gat agc act ggt aag ttt aaa gag ctg ata gga agt							561
Asp Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser							
	115		120		125		
agc ggt aag gac ata cta aaa aac att ctt aca gat agc acc ggt aag							609
Ser Gly Lys Asp Ile Leu Lys Asn Ile Leu Thr Asp Ser Thr Gly Lys							
	130		135		140		145
ttt aaa gaa ctt ata gaa agt gca ggt aag ggt aag ctg aaa gac ctt							657
Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys Gly Lys Leu Lys Asp Leu							
	150		155		160		
ctt att gat gga aac ttt aaa aaa tta ttt gag gat gac acg aaa gct							705
Leu Ile Asp Gly Asn Phe Lys Lys Leu Phe Glu Asp Asp Thr Lys Ala							
	165		170		175		
gct cat gta aaa gaa ata ctt aca gag agc aac gct aag gaa ata ctc							753
Ala His Val Lys Glu Ile Leu Thr Asp Ser Asn Ala Lys Glu Ile Leu							
	180		185		190		
aca aat gaa gta gca aaa gag gta cta aaa tcc gat aaa ttt aaa gat							801
Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser Asp Lys Phe Lys Asp							
	195		200		205		
gca ata act ggt gct ggt aag gac gca cta aaa gag ata ctt act tgc							849
Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys							
	210		215		220		225
gat aaa ttt aaa gat gca gta aca ggc aat ggt aag gac gca cta aaa							897
Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly Lys Asp Ala Leu Lys							
	230		235		240		
gaa ata ctt act tgc gat aaa ttt aaa gat gca gta aca ggc aat ggt							945
Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly							
	245		250		255		
aaa gac aag cta aaa gag att ctt act cac gag aag ttt aaa gca ctc							993
Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu Lys Phe Lys Ala Leu							

Untitled																
260				265				270								
ata	gag	agt	gaa	ggc	aaa	gac	ata	ctg	aaa	gac	att	ctt	aca	gat	agt	1041
Ile	Glu	Ser	Glu	Gly	Lys	Asp	Ile	Leu	Lys	Asp	Ile	Leu	Thr	Asp	Ser	
275																
acc	ggt	aaa	ttt	aaa	gag	cta	ata	gaa	agc	acg	ggt	aag	gat	gaa	gca	1089
Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Glu	Ser	Thr	Gly	Lys	Asp	Glu	Ala	
290																
aaa	gca	gta	ctt	act	gac	gag	aaa	ttt	aaa	gac	ttg	ttt	aat	gac	aaa	1137
Lys	Ala	Val	Leu	Thr	Asp	Glu	Lys	Phe	Lys	Asp	Leu	Phe	Asn	Asp	Lys	
310																
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Thr	Thr	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu	Thr	Ser	Asp	Lys	Phe	Lys	
325																
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Lys	Leu	Phe	Glu	Asp	Asn	Thr	Lys	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu	
340																
acg	aac	gat	aca	gct	aag	gaa	ata	ctt	acc	aat	cat	aaa	ttt	aag	gaa	1281
Thr	Asn	Asp	Thr	Ala	Lys	Glu	Ile	Leu	Thr	Asn	His	Lys	Phe	Lys	Glu	
355																
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370																
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390																
cta	aaa	tac	ata	ctc	act	aat	agc	gag	ttt	aaa	agc	tta	ttt	gat	agc	1425
Leu	Lys	Tyr	Ile	Leu	Thr	Asn	Ser	Glu	Phe	Lys	Ser	Leu	Phe	Asp	Ser	
405																
aaa	gat	agc	gct	gaa	gct	ggt	aaa	gaa	ata	ttt	acc	cac	agt	aag	ttt	1473
Lys	Asp	Ser	Ala	Glu	Ala	Val	Lys	Glu	Ile	Phe	Thr	His	Ser	Lys	Phe	
420																
aaa	gaa	cta	ctt	aaa	acg	tgc	aag	gac	aac	cca	aaa	aat	acg	gcg	gcg	1521
Lys	Glu	Leu	Leu	Lys	Thr	Cys	Lys	Asp	Asn	Pro	Lys	Asn	Thr	Ala	Ala	
435																
ctt	gca	gct	gct	tta	gat	gaa	cta	aaa	gat	cta	att	acc	tgt	ggc	agc	1569
Leu	Ala	Ala	Ala	Leu	Asp	Glu	Leu	Lys	Asp	Leu	Ile	Thr	Cys	Gly	Ser	
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ggt	gat	cat	gca	aca	aaa	cta	caa	gcc	ttt	gga	agt	gca	cta	tgc	acc	1617
Gly	Asp	His	Ala	Thr	Lys	Leu	Gln	Ala	Phe	Gly	Ser	Ala	Leu	Cys	Thr	
470																
aga	aaa	aaa	gag	tcg	tgc	gat	aat	ttt	agc	tct	gca	aac	tgc	agt	agt	1665
Arg	Lys	Lys	Glu	Ser	Cys	Asp	Asn	Phe	Ser	Ser	Ala	Asn	Cys	Ser	Ser	
485																
aca	aca	act	gca	taattacgta	gcgctagggtg	ggggtaattt	acccccacct									1717
Thr	Thr	Thr	Ala													

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	Leu	Thr	Asp	Ser	Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Gly	Ser	Ser	Gly		
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	Lys	Asp	Ile	Leu	Lys	Ser	Ile	Leu	Thr	Asp	Gly	Ser	Gly	Asn	Phe	Lys		
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	Gly	Leu	Ile	Gln	Ser	Thr	Gly	Lys	Ala	Glu	Val	Lys	Glu	Val	Leu	Thr		
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	Asn	Glu	Lys	Phe	Lys	Glu	Leu	Phe	Gly	Ser	Asp	Gly	Lys	Asp	Ile	Leu		
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	Lys	Asp	Ile	Leu	Thr	Asp	Ser	Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Gly		
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	Lys	Phe	Lys	Glu	Leu	Ile	Glu	Ser	Ala	Gly	Lys	Gly	Lys	Leu	Lys	Asp		
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	Leu	Leu	Ile	Asp	Gly	Asn	Phe	Lys	Lys	Leu	Phe	Glu	Asp	Asp	Thr	Lys		
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	Ala	Ala	His	Val	Lys	Glu	Ile	Leu	Thr	Asp	Ser	Asn	Ala	Lys	Glu	Ile		
				180					185					190				
	Leu	Thr	Asn	Glu	Val	Ala	Lys	Glu	Val	Leu	Lys	Ser	Asp	Lys	Phe	Lys		
			195					200					205					
	Asp	Ala	Ile	Thr	Gly	Ala	Gly	Lys	Asp	Ala	Leu	Lys	Glu	Ile	Leu	Thr		
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	Cys	Asp	Lys	Phe	Lys	Asp	Ala	Val	Thr	Gly	Asn	Gly	Lys	Asp	Ala	Leu		
			225			230				235					240			
	Lys	Glu	Ile	Leu	Thr	Cys	Asp	Lys	Phe	Lys	Asp	Ala	Val	Thr	Gly	Asn		
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	Leu	Ile	Glu	Ser	Glu	Gly	Lys	Asp	Ile	Leu	Lys	Asp	Ile	Leu	Thr	Asp		
			275					280					285					
	Ser	Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Glu	Ser	Thr	Gly	Lys	Asp	Glu		
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	Lys	Thr	Thr	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu	Thr	Ser	Asp	Lys	Phe		
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	Glu	Ala	Ile	Thr	Gly	Asp	Gly	Lys	Asp	Ile	Leu	Lys	Glu	Ile	Leu	Thr		
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	Gln	Leu	Lys	Tyr	Ile	Leu	Thr	Asn	Ser	Glu	Phe	Lys	Ser	Leu	Phe	Asp		
				405						410				415				
	Ser	Lys	Asp	Ser	Ala	Glu	Ala	Val	Lys	Glu	Ile	Phe	Thr	His	Ser	Lys		
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Untitled

Ser	Gly	Asp	His	Ala	Thr	Lys	Leu	Gln	Ala	Phe	Gly	Ser	Ala	Leu	Cys
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Thr	Arg	Lys	Lys	Glu	Ser	Cys	Asp	Asn	Phe	Ser	Ser	Ala	Asn	Cys	Ser
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